usl.res

32 20 K-tuple Joining penalty Window size PARAMETERS Unitary 1 1.00 0.05 Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group

SEARCH STATISTICS Median 7 Mean 18 Scores:

Standard Deviation 24.55

Total Elapsed 00:00:00:00

1084 6 6 00:00:00:00 Number of residues: Number of sequences searched: Number of scores above cutoff: Times:

The scores below are sorted by initial score.

Finitial score.

100% identical sequence to the query sequence was not found.

The list of best scores is:

ption Init. Opt. Length Score Score	:. ore Sig.	Frame
aa291397p_6 *** 1 standard deviation above mean **** aa291397p_6 **** 0 standard deviation from mos. ***	;	
1181 20 30 181 181 6 30 - 180 5 28 - 180 5 28 - 180 5 28 - 180	30 0.08 31 -0.41 30 -0.49	0000
(1-226)		
Initial Score 67 Optimized Score 70 Significance 2. Residue Identity 75% Matches 11 Conservative Substitution		
130 1 VWSRNEDITEPQSI	OAGGLLEK	20 120
1 1 1 1	20	9
TEKVKNOLKETTEAACRYGAFGLPITVAHVDGQTHMLFGSDRMELWRTCWERSGWALYLQPXMPDFKIA 30 40 50 60 60 70 80 80 80 90 90 90 90 90 90 90 90 90 90 90 90 90	4GPIPPAVN PDFKI	 ≤-«
X RL 	, ,	
RRKOTLRIKKAGHLLNPWLHHKALGLGFLYLIEVFSVALGAVCLSPTPKDAR X 100 120 130		